Amendments to the Specification

Please replace the paragraph on page 2, lines 8-24, with the following rewritten paragraph:

Thus, in a previous patent application (PCT/FR98/01442; which corresponds to U.S. Patent Application No. 09/446,024), the applicant screened a cDNA library using a Ppol-MSRV probe (SEQ ID NO. 18) and detected overlapping clones which allowed it to reconstruct a putative genomic RNA of 7582 nucleotides. This genomic RNA has an R-U5-gag-pol-env-U3-R structure. A "blastn" interrogation over several databases using the reconstructed genome made it possible to show that there is a considerable amount of related genomic (DNA) sequences in the human genome, which are found on several chromosomes. Thus, the applicant demonstrated the existence of partial structures of the retroviral type in the human genome and envisaged their potential role in the development of autoimmune diseases, in unsuccessful pregnancy or pathological conditions of pregnancy.

Please replace the paragraph on page 2, lines 31-36, with the following rewritten paragraph:

The isolation and sequencing of overlapping cDNA fragments and the identification of genomic (DNA) clones corresponding to the isolated DNA clones, described in the applicant's above-mentioned PCT and corresponding U.S. patent applications, are incorporated herein by way of reference.

Please replace the paragraph on page 6, lines 3-25, with the following rewritten paragraph:

The location of the aligned regions for each of the clones is indicated and the chromosome to which they belong is indicated between square brackets (Figure ~~6 [sic]~~3 of the above-mentioned PCT and corresponding U.S. application, which corresponds to Figure 1 herein). The percentage similarity (without the large deletions) between the 4 sequences and

the reconstructed genomic RNA is indicated, ~~and also~~ as well as the presence of repeat sequences at each end of the genome and the size of the longest open reading frames (ORFs). Repeat sequences were found at the ends of 3 of these clones. The reconstructed sequence is entirely contained within clone RG083M05 (9.6 Kb) and exhibits 96% similarity. However, clone RG083M05 has a 2 Kb insertion located immediately downstream of the 5' untranslated region (5' UTR). This insertion is also found in two other genomic clones which have a 2.3 Kb deletion immediately upstream of the 3' untranslated region (3' UTR). No clone contained the three functional gag, pol and env open reading frames (ORFs). Clone RG083M05 shows a 538 amino acid (AA) ORF corresponding to a whole envelope. Cosmid Q11M15 contains two major contiguous ORFs of 413 AA (frame 0) and 305 AA (frame +1) corresponding to a truncated pol polyprotein.

Please replace the paragraph on page 13, lines 6-10, with the following rewritten paragraph:

The clone obtained, named Cl2, makes it possible to define a 1511 bp region which has an open reading frame in the N-terminal region of 1056 bp (SEQ ID NO. 3) encoding ~~359~~ 352 amino acids ~~(SEQ ID NO. 31)~~ corresponding to the matrix and capsid regions of the *gag* gene.

Please replace the paragraph on page 18, line 34 through page 19, line 6, with the following rewritten paragraph:

By this process a 2009 bp fragment (SEQ ID NO: 2) was sequenced. The 1089 bp coding portion ~~encoded (SEQ ID NO. 31) by~~ of the 2009 bp fragment (fragment 434-1522 of SEQ ID NO. 2), which encodes the protein of SEQ ID NO: 31, was amplified by PCR with the *Pwo* enzyme (5 U/µl) (Boehringer Manneim, France) using 1 µl of the minipreparation of the gag clone DNA (SEQ ID NO. 3) under the following conditions: 95°C 1 min, 60°C 1 min and 72°C 2 min for 25 cycles, with a final reaction volume of 50 µl, using the primers:

_____- 5' primer (*Bam* HI) (SEQ ID NO. 8):

_____5' ATG GGA AAC GTT CCC CCC GAG 3' (21 mer), and

_____- 3' primer (*Hind* III), identified by SEQ ID NO. 9:

_____5'~~[sic]~~ GGC CTA AGG CAG ACT TTT GAA 3' (21 mer).

Please replace the paragraph on page 19, line 32 through page 20, line 4, with the following rewritten paragraph:

A mixture containing 12.5 µl of TNT® rabbit reticulocyte lysate (Promega), 1 µl of TNT® reaction buffer (Promega), 0.5 µl of TNT® RNA polymerase (Promega), 0.5 µl of a 1 mM mixture of amino acids minus methionine, 2 µl of ^{35}S-methionine (1000 Ci/mmol) at 10 mCi/µl (Amersham), 0.5 µl of RNasin® ribonuclease inhibitor at 40 U/µl, 4 µl of PCR amplification products (equivalent to 1 µg) from each human chromosome and 4 µl of water, in a reaction volume of 25 µl~~, [lacuna]~~. This mixture was incubated at 30°C for 90 min.

Please replace the paragraph on page 22, lines 4-7, with the following rewritten paragraph:

The coding region of SEQ ID NO. 2 was expressed in *Escherichia coli*, and then the products thus expressed were tested against serum from patients suffering from MS, and also against serum from healthy patients.